What is claimed is:

1. A recombinant nucleic acid molecule comprising a heterologous nucleic acid coding sequence encoding a plant long chain fatty acid condensing enzyme, wherein:

a) the nucleic acid coding sequence is derived from an *Arabidopsis KCS2* coding sequence; or

b) the plant very long chain fatty acid condensing enzyme catalyses the condensation of malonyl-CoA with a C16, C18, C20 or C22 acyl-CoA, wherein the plant very long chain fatty acid condensing enzyme has an amino acid sequence that is at least 70% identical to an *Arabidopsis* KCS2 amino acid sequence when optimally aligned; or

c) the nucleic acid coding sequence hybridizes under stringent conditions to a complement of the *Arabidopsis KCS2* coding sequence; or

d) the nucleic acid coding sequence at least 70% identical to the *Arabidopsis KCS2* coding sequence when optimally aligned.

2. The recombinant nucleic acid molecule of claim 1 wherein the nucleic acid coding sequence is derived from the *Arabidopsis KCS2* coding sequence.

3. The recombinant nucleic acid molecule of claim 1 wherein the plant very long chain fatty acid condensing enzyme catalyses the condensation of malonyl-CoA with a C16, C18, C20 or C22 acyl-CoA, wherein the plant very long chain fatty acid condensing enzyme has an amino acid sequence that is at least 70% identical to the *Arabidopsis* KCS2 amino acid sequence when optimally aligned.

4. The recombinant nucleic acid molecule of claim 1 wherein the nucleic acid coding sequence hybridizes under stringent conditions to the complement of the *Arabidopsis KCS2* coding sequence.

5. The recombinant nucleic acid molecule of claim 1 wherein the nucleic acid coding sequence at least 70% identical to the *Arabidopsis KCS2* coding sequence when optimally aligned.

6. The recombinant nucleic acid molecule of claim 1 wherein the nucleic acid coding sequence at least 90% identical to a wild-type *Arabidopsis KCS2* coding sequence when optimally aligned.

7. The recombinant nucleic acid molecule of claim 1 wherein the nucleic acid coding sequence at least 95% identical to a wild-type *Arabidopsis KCS2* coding sequence when optimally aligned.

8. An isolated nucleic acid molecule comprising a nucleic acid coding sequence that encodes a plant long chain fatty acid condensing enzyme, wherein:

a) the nucleic acid coding sequence is derived from an *Arabidopsis KCS2* coding sequence; or

b) the plant long chain fatty acid condensing enzyme catalyses the condensation of malonyl-CoA with a C16, C18, C20 or C22 acyl-CoA, wherein the plant very long chain fatty acid condensing enzyme has an amino acid sequence that is at least 70% identical to an *Arabidopsis* KCS2 amino acid sequence when optimally aligned; or

c) the nucleic acid coding sequence hybridizes under stringent conditions to a complement of the *Arabidopsis KCS2* coding sequence; or

d) the nucleic acid coding sequence is at least 70% identical to the *Arabidopsis KCS2* coding sequence when optimally aligned.

9. The isolated nucleic acid molecule of claim 8, wherein the nucleic acid coding sequence is derived from the *Arabidopsis KCS2* coding sequence.

10. The isolated nucleic acid molecule of claim 8, wherein the plant long chain fatty acid condensing enzyme catalyses the condensation of malonyl-CoA with a C16, C18, C20 or C22 acyl-CoA, wherein the plant very long chain fatty acid condensing enzyme has an amino acid sequence that is at least 70% identical to an *Arabidopsis* KCS2 amino acid sequence when optimally aligned.

11. The isolated nucleic acid molecule of claim 8, wherein the nucleic acid coding sequence hybridizes under stringent conditions to a complement of the *Arabidopsis KCS2* coding sequence.

12. The isolated nucleic acid molecule of claim 8, wherein the nucleic acid coding sequence is at least 70% identical to the *Arabidopsis KCS2* coding sequence when optimally aligned.

13. The isolated nucleic acid molecule of claim 8, wherein the nucleic acid coding sequence is at least 90% identical to a wild-type *Arabidopsis KCS2* coding sequence when optimally aligned.

14. The isolated nucleic acid molecule of claim 8, wherein the nucleic acid coding sequence is at least 95% identical to a wild-type *Arabidopsis KCS2* coding sequence when optimally aligned.

15. A recombinant nucleic acid molecule comprising a promoter sequence operably linked to a nucleic acid sequence, wherein the promoter sequence is capable of mediating gene expression in anthers and in very young leaves in *Arabidopsis* and:

a) is derived from an *Arabidopsis KCS2* promoter sequence; or

b) hybridizes under stringent conditions to the *Arabidopsis KCS2* promoter sequence; or,

c) is at least 70% identical to the *Arabidopsis KCS2* promoter sequence when optimally aligned.

16. The recombinant nucleic acid molecule of claim 15, wherein the promoter sequence is derived from the *Arabidopsis KCS2* promoter sequence.

17. The recombinant nucleic acid molecule of claim 15, wherein the promoter sequence hybridizes under stringent conditions to the *Arabidopsis KCS2* promoter sequence.

18. The recombinant nucleic acid molecule of claim 15, wherein the promoter sequence is at least 70% identical to the *Arabidopsis KCS2* promoter sequence when optimally aligned.

19. The recombinant nucleic acid molecule of claim 15, wherein the promoter sequence is at least 90% identical to a wild-type *Arabidopsis KCS2* promoter sequence when optimally aligned.

20. A nucleic acid probe comprising a probe sequence that:

a) hybridizes under stringent conditions to a portion of an Arabidopsis *KCS2* genomic sequence; or

b) is at least 70% identical to the portion of an Arabidopsis *KCS2* genomic sequence when optimally aligned.

21. The nucleic acid probe of claim 20 wherein the probe sequence hybridizes under stringent conditions to a portion of the Arabidopsis *KCS2* genomic sequence.

22. The nucleic acid probe of claim 20 wherein the probe sequence is at least 70% identical to the portion of the Arabidopsis *KCS2* genomic sequence when optimally aligned.

23. The nucleic acid probe of claim 20 wherein the probe sequence is at least 90% identical to a portion of a wild-type Arabidopsis *KCS2* genomic sequence when optimally aligned.

24. A transgenic plant comprising the recombinant nucleic acid molecule of any one of claims 1 through 7.

25. A part of the transgenic plant of claim 24.

26. The part of the transgenic plant of claim 25, wherein the part is a seed.

27. The transgenic plant of claim 24, wherein the transgenic plant has a modified phenotype compared to a non-transgenic plant of the same species.

28. A transgenic cell comprising the recombinant nucleic acid molecule of any one of claims 1 through 7.

29. The transgenic cell of claim 28, wherein the cell is a plant cell.

30. A method of producing a transgenic plant comprising introducing into the plant the isolated nucleic acid molecule of any one of claims 8 through 14.

31. A progeny plant produced by sexual or asexual propagation of the transgenic plant produced by the method of claim 30.

32. A purified protein encoded by the recombinant nucleic acid molecule of any one of claims 1 through 7.

33. A recombinant vector comprising the recombinant nucleic acid molecule of any one of claims 1 through 7.

34. A recombinant antisense nucleic acid molecule wherein a portion of the heterologous nucleic acid coding sequence of claim 1 is in reverse orientation relative to an adjacent promoter sequence.

35. The recombinant antisense nucleic acid of claim 34, wherein the recombinant antisense nucleic acid encodes an antisense RNA that:

a) hybridizes under stringent conditions to a complement of a portion of the *Arabidopsis KCS2* coding sequence; or

b) is at least 70% identical to a portion of the *Arabidopsis KCS2* coding sequence when optimally aligned.

36. A Transgenic plant or plant cell comprising the recombinant antisense nucleic acid of claim 34 or 35.

37. A method of isolating a nucleic acid molecule encoding a plant long chain fatty acid condensing enzyme, the method comprising hybridizing a nucleic acid preparation with the nucleic acid probe of any one of claims 20 through 23.